

#11

8/15



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ENTERED

RAW SEQUENCE LISTING

DATE: 08/14/2002

PATENT APPLICATION: US/09/993,756D

TIME: 14:45:06

Input Set : A:\pf01113con_subseqlist.txt

Output Set: N:\CRF4\08142002\I993756D.raw

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1 <110> APPLICANT: Bailleul, Bernard
2      Strosberg, A. Donny
3      Akerblom, Ingrid E.
5 <120> TITLE OF INVENTION: HUMAN LEPTIN RECEPTOR GENE-RELATED PROTEIN
7 <130> FILE REFERENCE: PF-0111-3 CON
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/993,756D
C--> 10 <141> CURRENT FILING DATE: 2002-08-09
12 <160> NUMBER OF SEQ ID NOS: 4
13 <170> SOFTWARE: PERL Program
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 131
17 <212> TYPE: PRT
18 <213> ORGANISM: Homo sapiens
20 <220> FEATURE:
21 <221> NAME/KEY: misc_feature
22 <223> OTHER INFORMATION: Incyte ID No: 492703
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27 Ile Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr
28                      20                      25                      30
29 Gly Val Tyr Trp Pro Leu Phe Val Leu Ile Phe His Gly Ile Ser
30                      35                      40                      45
31 Pro Ile Pro His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp
32                      50                      55                      60
33 Ala Thr Ser Ser Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr
34                      65                      70                      75
35 Gly Ile Val Val Ser Ala Phe Gly Phe Pro Val Ile Leu Ala Arg
36                      80                      85                      90
37 Val Ala Val Ile Lys Trp Gly Ala Cys Gly Leu Val Leu Ala Gly
38                      95                      100                     105
39 Asn Ala Val Ile Phe Leu Thr Ile Gln Gly Phe Phe Leu Ile Phe
40                      110                     115                     120
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42                      125                     130
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45 <211> LENGTH: 874
46 <212> TYPE: PRT
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49 <220> FEATURE:
50 <221> NAME/KEY: misc_feature
51 <223> OTHER INFORMATION: Incyte ID No: 492703
53 <400> SEQUENCE: 2

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54	Gly	Thr	Cys	Thr	Gly	Gly	Cys	Thr	Thr	Gly	Gly	Gly	Cys	Ala	Gly
55	1				5					10					15
56	Gly	Cys	Thr	Gly	Cys	Cys	Cys	Gly	Gly	Gly	Cys	Cys	Gly	Thr	Gly
57					20					25					30
58	Gly	Cys	Ala	Gly	Gly	Ala	Ala	Gly	Cys	Ser	Gly	Gly	Ala	Ala	Gly
59					35					40					45
60	Cys	Ala	Gly	Cys	Cys	Gly	Cys	Gly	Gly	Cys	Cys	Cys	Cys	Ala	Gly
61					50					55					60
62	Thr	Thr	Cys	Gly	Gly	Gly	Ala	Gly	Ala	Cys	Ala	Thr	Gly	Gly	Cys
63					65					70					75
64	Gly	Gly	Gly	Cys	Gly	Thr	Thr	Ala	Ala	Ala	Gly	Cys	Thr	Cys	Thr
65					80					85					90
66	Cys	Gly	Thr	Gly	Gly	Cys	Ala	Thr	Thr	Ala	Thr	Cys	Cys	Thr	Thr
67					95					100					105
68	Cys	Ala	Gly	Thr	Gly	Gly	Gly	Gly	Cys	Thr	Ala	Thr	Thr	Gly	Gly
69					110					115					120
70	Ala	Cys	Thr	Gly	Ala	Cys	Thr	Thr	Thr	Thr	Cys	Thr	Thr	Ala	Thr
71					125					130					135
72	Gly	Cys	Thr	Gly	Gly	Gly	Ala	Thr	Gly	Thr	Gly	Cys	Cys	Thr	Thr
73					140					145					150
74	Ala	Gly	Ala	Gly	Gly	Ala	Thr	Thr	Ala	Thr	Gly	Gly	Cys	Gly	Thr
75					155					160					165
76	Thr	Thr	Ala	Cys	Thr	Gly	Gly	Cys	Cys	Cys	Thr	Thr	Ala	Thr	Thr
77					170					175					180
78	Cys	Gly	Thr	Cys	Cys	Thr	Gly	Ala	Thr	Thr	Thr	Thr	Cys	Cys	Ala
79					185					190					195
80	Cys	Gly	Gly	Cys	Ala	Thr	Cys	Thr	Cys	Cys	Cys	Cys	Cys	Ala	Thr
81					200					205					210
82	Cys	Cys	Cys	Cys	Cys	Ala	Thr	Thr	Thr	Cys	Ala	Thr	Thr	Gly	Cys
83					215					220					225
84	Cys	Ala	Ala	Ala	Ala	Gly	Ala	Gly	Thr	Cys	Ala	Cys	Cys	Thr	Ala
85					230					235					240
86	Thr	Gly	Ala	Cys	Thr	Cys	Ala	Gly	Ala	Thr	Gly	Cys	Ala	Ala	Cys
87					245					250					255
88	Cys	Ala	Gly	Thr	Ala	Gly	Thr	Gly	Cys	Cys	Thr	Gly	Thr	Cys	Gly
89					260					265					270
90	Gly	Gly	Ala	Ala	Cys	Thr	Gly	Gly	Cys	Ala	Thr	Ala	Thr	Thr	Thr
91					275					280					285
92	Cys	Thr	Thr	Cys	Ala	Cys	Thr	Ala	Cys	Thr	Gly	Gly	Ala	Ala	Thr
93					290					295					300
94	Thr	Gly	Thr	Thr	Gly	Thr	Thr	Thr	Cys	Thr	Gly	Cys	Cys	Thr	Thr
95					305					310					315
96	Thr	Gly	Gly	Ala	Thr	Thr	Thr	Cys	Cys	Thr	Gly	Thr	Thr	Ala	Thr
97					320					325					330
98	Thr	Cys	Thr	Thr	Gly	Cys	Thr	Cys	Gly	Thr	Gly	Thr	Gly	Gly	Cys
99					335					340					345
100	Thr	Gly	Thr	Gly	Ala	Thr	Cys	Ala	Ala	Ala	Thr	Gly	Gly	Gly	Gly
101					350					355					360
102	Ala	Gly	Cys	Cys	Thr	Gly	Cys	Gly	Gly	Cys	Cys	Thr	Thr	Gly	Thr

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103					365					370				375	
104	Gly	Thr	Thr	Gly	Gly	Cys	Ala	Gly	Gly	Cys	Ala	Ala	Thr	Gly	Cys
105					380					385				390	
106	Ala	Gly	Thr	Cys	Ala	Thr	Thr	Thr	Thr	Cys	Cys	Thr	Thr	Ala	Cys
107					395					400				405	
108	Ala	Ala	Thr	Thr	Cys	Ala	Ala	Gly	Gly	Gly	Thr	Thr	Thr	Thr	Thr
109					410					415				420	
110	Cys	Cys	Thr	Thr	Ala	Thr	Ala	Thr	Thr	Thr	Gly	Gly	Ala	Ala	Gly
111					425					430				435	
112	Ala	Gly	Gly	Ala	Gly	Ala	Thr	Gly	Ala	Thr	Thr	Thr	Thr	Ala	Gly
113					440					445				450	
114	Cys	Thr	Gly	Gly	Gly	Ala	Gly	Cys	Ala	Gly	Thr	Gly	Gly	Thr	Ala
115					455					460				465	
116	Gly	Cys	Ala	Cys	Thr	Thr	Thr	Ala	Thr	Thr	Cys	Thr	Gly	Ala	Thr
117					470					475				480	
118	Thr	Ala	Cys	Ala	Gly	Thr	Gly	Cys	Ala	Thr	Thr	Gly	Ala	Ala	Thr
119					485					490				495	
120	Thr	Thr	Cys	Thr	Thr	Ala	Gly	Ala	Ala	Cys	Thr	Cys	Ala	Thr	Ala
121					500					505				510	
122	Cys	Thr	Ala	Thr	Cys	Thr	Gly	Thr	Ala	Thr	Ala	Cys	Ala	Thr	Gly
123					515					520				525	
124	Thr	Gly	Cys	Ala	Cys	Ala	Thr	Gly	Cys	Gly	Gly	Cys	Ala	Thr	Thr
125					530					535				540	
126	Thr	Thr	Ala	Cys	Thr	Ala	Thr	Gly	Ala	Ala	Ala	Thr	Thr	Thr	Ala
127					545					550				555	
128	Ala	Thr	Ala	Thr	Gly	Cys	Thr	Gly	Gly	Gly	Thr	Thr	Thr	Thr	Thr
129					560					565				570	
130	Thr	Ala	Ala	Thr	Ala	Cys	Cys	Thr	Thr	Thr	Ala	Thr	Ala	Thr	Ala
131					575					580				585	
132	Thr	Cys	Ala	Thr	Gly	Thr	Thr	Cys	Ala	Cys	Thr	Thr	Thr	Ala	Ala
133					590					595				600	
134	Gly	Ala	Ala	Ala	Gly	Ala	Cys	Thr	Thr	Cys	Ala	Thr	Ala	Ala	Gly
135					605					610				615	
136	Thr	Ala	Gly	Gly	Ala	Gly	Ala	Thr	Gly	Ala	Gly	Thr	Thr	Thr	Thr
137					620					625				630	
138	Ala	Thr	Thr	Cys	Thr	Cys	Ala	Gly	Cys	Ala	Ala	Ala	Thr	Ala	Gly
139					635					640				645	
140	Ala	Cys	Cys	Thr	Gly	Thr	Cys	Ala	Ala	Ala	Thr	Thr	Thr	Ala	Gly
141					650					655				660	
142	Ala	Thr	Thr	Ala	Thr	Gly	Thr	Thr	Ala	Cys	Thr	Cys	Ala	Ala	Ala
143					665					670				675	
144	Thr	Thr	Ala	Thr	Gly	Thr	Thr	Ala	Cys	Thr	Thr	Gly	Thr	Thr	Thr
145					680					685				690	
146	Gly	Gly	Cys	Thr	Gly	Thr	Thr	Cys	Ala	Thr	Gly	Thr	Ala	Gly	Thr
147					695					700				705	
148	Cys	Ala	Cys	Gly	Gly	Thr	Gly	Cys	Thr	Cys	Thr	Cys	Ala	Gly	Ala
149					710					715				720	
150	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr	Thr	Ala	Ala	Cys	Gly	Cys	Ala
151					725					730				735	

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152 Gly Thr Cys Thr Thr Gly Thr Ala Gly Gly Cys Ala Gly Cys Thr
153                               740                               745                               750
154 Gly Cys Cys Ala Cys Cys Thr Thr Ala Thr Gly Cys Ala Gly Thr
155                               755                               760                               765
156 Gly Cys Ala Thr Cys Gly Ala Ala Ala Cys Cys Thr Thr Thr Thr
157                               770                               775                               780
158 Gly Cys Thr Thr Gly Gly Gly Gly Ala Thr Gly Thr Gly Cys Thr
159                               785                               790                               795
160 Thr Gly Gly Ala Gly Ala Gly Gly Cys Ala Gly Ala Thr Ala Ala
161                               800                               805                               810
162 Cys Gly Cys Thr Gly Ala Ala Gly Cys Ala Gly Gly Cys Cys Thr
163                               815                               820                               825
164 Cys Thr Cys Ala Thr Gly Ala Cys Cys Cys Ala Gly Gly Ala Ala
165                               830                               835                               840
166 Gly Gly Cys Cys Gly Gly Gly Gly Thr Gly Gly Trp Thr Cys Cys
167                               845                               850                               855
168 Cys Thr Cys Thr Thr Thr Lys Thr Thr Thr Thr Gly Thr Ala Gly
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173 <210> SEQ ID NO: 3
174 <211> LENGTH: 145
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
178 <220> FEATURE:
179 <221> NAME/KEY: misc_feature
180 <223> OTHER INFORMATION: GenBank ID No: g733888
182 <400> SEQUENCE: 3
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185 Lys Asn Thr Ile Leu Ala Val Ala Ala Leu Ala Phe Ala Gly Val
186                               20                               25                               30
187 Val Gly Leu Thr Phe Leu Val Leu Gly Cys Ala Leu Pro Arg Tyr
188                               35                               40                               45
189 Gly Thr Trp Thr Pro Met Phe Val Ile Thr Phe Tyr Val Leu Ser
190                               50                               55                               60
191 Pro Val Pro Leu Leu Ile Ala Arg Arg Phe Gln Glu Asp Met Thr
192                               65                               70                               75
193 Gly Thr Asn Ala Cys Ile Glu Leu Ala Leu Phe Ile Thr Thr Gly
194                               80                               85                               90
195 Ile Val Ile Ser Ala Phe Ala Leu Pro Ile Val Leu Ala His Ala
196                               95                               100                              105
197 Gly Thr Ile Ala Met Ser Ala Cys Phe Leu Ile Phe Ile Ala Asn
198                               110                              115                              120
199 Ser Ile Asn Phe Ser Val Ile Ile Phe Tyr Phe Arg Ile Phe Asn
200                               125                              130                              135
201 Gly Glu Asp Met Asn Gly Met Ser Leu Trp
202                               140                              145
204 <210> SEQ ID NO: 4
205 <211> LENGTH: 140

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206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
209 <220> FEATURE:
210 <221> NAME/KEY: misc_feature
211 <223> OTHER INFORMATION: GenBank ID No: g1197072
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217           20           25           30
218 Ala Leu Phe His Asn Tyr Tyr Pro Leu Phe Asp Ile Leu Ile Phe
219           35           40           45
220 Leu Leu Ala Pro Ile Pro Asn Thr Ile Phe Asn Ala Gly Asn Lys
221           50           55           60
222 Tyr His Thr Ser Asp Phe Met Ser Asp Ser Ser Asn Thr Gly Gln
223           65           70           75
224 Asp Leu Ala His Phe Leu Thr Gly Met Leu Val Thr Ser Gly Ile
225           80           85           90
226 Ala Leu Pro Val Val Phe Tyr His Cys Gln Leu Ile Gly His Leu
227           95          100          105
228 Ser Cys Ile Met Cys Met Ile Gly Gly Leu Ile Ile Tyr Ser Ser
229          110          115          120
230 Ile Val Ile Phe Lys Trp Phe Phe Lys Lys Asp Phe Asn Glu Asp
231          125          130          135
232 Asp Ser Leu Phe Gly
233          140

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VERIFICATION SUMMARY

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Input Set : A:\pf01113con_subseqlist.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date